GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 08:54:47 ; Search time 242.002 Seconds
(without alignments)
8273.863 Million cell updates/sec

Title: US-09-963-521-1
Perfect score: 2817
Sequence: 1 aatgaaataatccccctcacc.....tgatctgttccgtcagctgc 2817

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2817	100.0	2817	4	US-09-431-099-1	Sequence 1, Appli
	2	1836.6	65.2	1909	4	US-09-431-099-3	Sequence 3, Appli
	3	1561.2	55.4	1590	4	US-09-602-787A-557	Sequence 557, App
	4	157.8	5.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	5	157.8	5.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	6	149.4	5.3	36138	4	US-08-311-731A-136	Sequence 136, App
	7	72.2	2.6	536165	4	US-09-214-808-1	Sequence 1, Appli
	8	71.6	2.5	1446	2	US-08-569-150A-2	Sequence 2, Appli
	9	71.6	2.5	2868	3	US-08-274-121B-1	Sequence 1, Appli
	10	70.2	2.5	1479	4	US-09-489-039A-7037	Sequence 7037, Ap
	11	56	2.0	1455	4	US-09-328-352-595	Sequence 595, App
	12	54.8	1.9	2241	4	US-09-248-796A-3169	Sequence 3169, Ap
	13	52.6	1.9	3165	4	US-09-614-221A-160	Sequence 160, App
	14	48	1.7	654	4	US-09-651-169A-36	Sequence 36, Appl
	15	47.6	1.7	7218	1	US-08-232-463-14	Sequence 14, Appl
	16	45.8	1.6	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	17	45.6	1.6	381	4	US-08-956-171E-4023	Sequence 4023, Ap
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c	20	44.8	1.6	400	4	US-08-781-986A-4234	Sequence 4234, Ap
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	22	44.8	1.6	3000	1	US-08-290-301-3	Sequence 3, Appli
	23	44.8	1.6	3000	3	US-09-013-598-3	Sequence 3, Appli
	24	44.8	1.6	5981	1	US-08-290-301-83	Sequence 83, Appl
	25	44.8	1.6	5981	3	US-09-013-598-83	Sequence 83, Appl
c	26	44.6	1.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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	33	44.4	1.6	239	4	US-08-781-986A-4544	Sequence 4544, Ap
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	37	44.4	1.6	400	4	US-08-781-986A-3631	Sequence 3631, Ap
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	45	44.4	1.6	6591	4	US-08-781-986A-3114	Sequence 3114, Ap

ALIGNMENTS

RESULT 1
US-09-431-099-1
; Sequence 1, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT: Degussa-HOls AG
; APPLICANT: Forschungszentrum-JOlich GmbH
; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-431-099-1

Query Match 100.0%; Score 2817; DB 4; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
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Qy         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
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Qy        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
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Qy        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
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Qy        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
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Qy        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
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Qy        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
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Db        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
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Db       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
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Qy       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
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Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
Db       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
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Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
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Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
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Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
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Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
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Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
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Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
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Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
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Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 2
US-09-431-099-3
; Sequence 3, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
;  APPLICANT:  Degussa-HOls AG
;  APPLICANT:  Forschungszentrum-JOlich GmbH
;  TITLE OF INVENTION:  New nucleotide sequences coding for the thrE gene and process fo
;  TITLE OF INVENTION:  enzymatic production of L-threonine with coryneform bacteria.
;  FILE REFERENCE:  990079 BT
;  CURRENT APPLICATION NUMBER: US/09/431,099
;  CURRENT FILING DATE:  1999-11-01
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum ATCC13032
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
US-09-431-099-3

  Query Match             65.2%;  Score 1836.6;  DB 4;  Length 1909;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

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Qy        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
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Db        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Db        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
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Db        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
              | |||||||| |||||||||| |||||||||||||| ||  ||||||| ||||| ||||
Db        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577

Qy        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
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Qy        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
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Db        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

Qy        816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
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Qy        876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935
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Db        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy        996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

Qy       1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
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Db       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Db       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Db       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Db       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Db       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Db       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Db       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy       2016 GCCGGTG 2022

Db       1898 GCCGGGG 1904
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RESULT 3
US-09-602-787A-557
; Sequence 557, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr"ger, Burkhard
; APPLICANT: Sch"der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-09-602-787A-557

Query Match 55.4%; Score 1561.2; DB 4; Length 1590;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy        298 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 357

Db          1 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 60

Qy        358 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 417

Db         61 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 120

Qy        418 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 477

Db        121 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 180

Qy        478 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 537
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Db        181 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 240

Qy        538 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGC 597
              |||||||||||||||||||||||||||||||| ||||| |||||||| ||||||||||
Db        241 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy        598 GGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCAC 657
              ||||||||||||||| ||  ||||||| ||||| ||||||||||||||||||||||||||
Db        301 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 360

Qy        658 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGG 717
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        361 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG 420

Qy        718 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 480

Qy        778 GGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCC 837
              ||||||||| |||||||||||||||||||||||||| |||||||||||||||||||| ||
Db        481 GGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCC 540

Qy        838 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGC 897
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        541 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGC 600

Qy        898 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 660

Qy        958 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy       1018 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy       1078 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 840

Qy       1138 GACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACG 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACG 900

Qy       1198 ATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 1257
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 960

Qy       1258 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1020

Qy       1318 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1080

Qy       1378 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1140

Qy       1438 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1200

Qy       1498 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1260

Qy       1558 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1261 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1320

Qy       1618 CACCTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1677
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1380

Qy       1678 TTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1440

Qy       1738 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1500

Qy       1798 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAA 1857
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1501 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAA 1560

Qy       1858 TAAAAGGTAAAAATCAACCTGCTTAGGCGT 1887
              |||||||||||||||||||||||||||||
Db       1561 TAAAAGGTAAAAATCAACCTGCTTAGGCGT 1590
```

RESULT 4
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 5.6%; Score 157.8; DB 3; Length 4403765;
Best Local Similarity 58.2%; Pred. No. 2.1e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

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Qy        2306 CTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATATGACTGTCCACCCAGATGGTAGCTA 2365
               ||| || || || || || || ||||| || ||| ||      | || || || |||
Db     3902073 CTTCGTGGTGGTAGCCAATCGACTGCCCGTCGATCTGGAGCGTCTTCCCGACGGCAGCAC 3902132

Qy        2366 TAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGGGGCTTTCCCCCGTTCTGGAACAACA 2425
               | |      | |||||||||| ||| | ||||| |   |     || || |||   | |
Db     3902133 AACCTGGAAACGCAGCCCCGGAGGCTTGGTCACCGCCTTGGAGCCGGTGCTGCGGCGTCG 3902192

Qy        2426 TCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAAC 2485
               || ||     |||||||| ||||| ||    |   || |  |   |||||||     |
Db     3902193 GCGCGGGGCCTGGGTCGGCTGGCCCGGCGTTAACGACGACGGGGCCGAACCCGACCTCCA 3902252

Qy        2486 AGATACGGGTG----------------------TTTTGCTGCACCCTGTTGTCCTCACTGC 2524
               |    ||  |                      |   || || || ||    || |  |
Db     3902253 CGTGCTGGACGGCCCCATCATCCAAGACGAGCTGGAACTTCATCCGGTACGGCTGAGCAC 3902312

Qy        2525 AAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCA 2584
               |  |||   |     | |||||||||| || || ||||| || |||||||| || | |||
Db     3902313 CACGGACATAGCTCAGTACTACGAGGGATTCTCCAACGCCACACTGTGGCCGCTGTACCA 3902372
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Qy       2585 CGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAA 2644
Db    3902373 CGACGTCATCGTCAAGCCGCTCTACCACCGCGAATGGTGGGATCGCTACGTCGACGTCAA 3902432

Qy       2645 CCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCA 2704
Db    3902433 CCAGCGCTTTGCCGAGGCCGCGTCGCGCGCCGCCGCCCACGGCGCAACCGTGTGGGTACA 3902492

Qy       2705 GGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGAT 2764
Db    3902493 GGACTACCAGCTGCAGCTGGTACCGAAGATGCTGCGCATGCTGCGGCCCGATCTGACCAT 3902552

Qy       2765 CGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db    3902553 CGGTTTCTTTTTGCACATCCCGTTCCCGCCGGTAGAGCTGTTTATGCAGATGC 3902605
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RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.6%; Score 157.8; DB 3; Length 4411529;
Best Local Similarity 58.2%; Pred. No. 2.1e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

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Qy       2306 CTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATATGACTGTCCACCCAGATGGTAGCTA 2365
Db    3908294 CTTCGTGGTGGTAGCCAATCGACTGCCCGTCGATCTGGAGCGTCTTCCCGACGGCAGCAC 3908353

Qy       2366 TAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGGGGCTTTCCCCCGTTCTGGAACAACA 2425
Db    3908354 AACCTGGAAACGCAGCCCCGGAGGCTTGGTCACCGCCTTGGAGCCGGTGCTGCGGCGTCG 3908413

Qy       2426 TCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAAC 2485
Db    3908414 GCGCGGGGCCTGGGTCGGCTGGCCCGGCGTTAACGACGACGGGGCCGAACCCGACCTCCA 3908473

Qy       2486 AGATACGGGTG----------TTTTGCTGCACCCTGTTGTCCTCACTGC 2524
Db    3908474 CGTGCTGGACGGCCCCATCATCCAAGACGAGCTGGAACTTCATCCGGTACGGCTGAGCAC 3908533

Qy       2525 AAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCA 2584
Db    3908534 CACGGACATAGCTCAGTACTACGAGGGATTCTCCAACGCCACACTGTGGCCGCTGTACCA 3908593

Qy       2585 CGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAA 2644
Db    3908594 CGACGTCATCGTCAAGCCGCTCTACCACCGCGAATGGTGGGATCGCTACGTCGACGTCAA 3908653

Qy       2645 CCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCA 2704
Db    3908654 CCAGCGCTTTGCCGAGGCCGCGTCGCGCGCCGCCGCCCACGGCGCAACCGTGTGGGTACA 3908713

Qy       2705 GGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGAT 2764
Db    3908714 GGACTACCAGCTGCAGCTGGTACCGAAGATGCTGCGCATGCTGCGGCCCGATCTGACCAT 3908773

Qy       2765 CGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db    3908774 CGGTTTCTTTTTGCACATCCCGTTCCCGCCGGTAGAGCTGTTTATGCAGATGC 3908826
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RESULT 6
US-08-311-731A-136
; Sequence 136, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36138 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-136

Query Match 5.3%; Score 149.4; DB 4; Length 36138;
Best Local Similarity 57.1%; Pred. No. 2.7e-37;
Matches 301; Conservative 0; Mismatches 211; Indels 15; Gaps 1;

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Qy       2306 CTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATATGACTGTCCACCCAGATGGTAGCTA 2365
Db      27896 CTTTGTAGTGGTCGCCAATCGCCTGCCAGTTGATCAGGTGCGACTTCCCGATGGCACTGC 27955

Qy       2366 TAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGGGGCTTTCCCCCGTTCTGGAACAACA 2425
Db      27956 GATCTGGAAGCGCAGTCCAGGCGGGTTGGTCACAGCGCTAGAGCCGCTGCTGCGTCAGCG 28015

Qy       2426 TCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAAC 2485
Db      28016 GCGCGGGGCCTGGGTCGGCTGGCCGGGCGTAATAAACGACAACGTGGACCTCGACTTGAC 28075

Qy       2486 AGATACG--------------GGTGTTTTGCTGCACCCTGTTGTCCTCACTGCAAGTGA 2530
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Db      28076 CATCAAGTCGATCGTGCAGGATGGCCTTACTCTTTATCCGGTACGGCTGAACACACATGA 28135

Qy       2531 CTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACGATTT 2590

Db      28136 TGTCGCCGAGTACTACGAGGGGTTCTCGAACGCCACGCTGTGGCCGCTATACCACGACGT 28195

Qy       2591 GATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCAA 2650

Db      28196 CATCGTAAAGCCCATTTACCACTGCGAATGGTGGGAACGCTACGTCGATGTCAACCGGCG 28255

Qy       2651 GTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGACTA 2710

Db      28256 CTTCGCCGAAACAACGTCACGCACAGCCGCCTACGGTGGGACCGTATGGGTGCAGGACTA 28315

Qy       2711 TCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTT 2770

Db      28316 CCAACTGCAATTGGTACCGAAGATGCTGCGCATAATGCGGCCCGACTTGACCATCGGTTT 28375

Qy       2771 CTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817

Db      28376 CTTCTTGCACATCCCGTTCCCGCCGGTGGAGCTGTTCATGCAGATAC 28422


RESULT 7
US-09-214-808-1
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
;  APPLICANT:  Rosenthal, Andre
;  APPLICANT:  Freiberg, Christoph
;  APPLICANT:  Perret, Xavier Philippe
;  APPLICANT:  Broughton, William John
;  TITLE OF INVENTION:  Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; Patent No. 6475793
;  TITLE OF INVENTION:  Plasmid
;  FILE REFERENCE:  CARP0068
;  CURRENT APPLICATION NUMBER: US/09/214,808A
;  CURRENT FILING DATE:  1999-06-22
;  PRIOR APPLICATION NUMBER:  PCT/IB97/00950
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  1
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 536165
;   TYPE: DNA
;   ORGANISM: Rhizobium
US-09-214-808-1

  Query Match             2.6%;  Score 72.2;  DB 4;  Length 536165;
  Best Local Similarity   52.5%;  Pred. No. 1.1e-10;
  Matches  158;  Conservative    0;  Mismatches  143;  Indels    0;  Gaps    0;

Qy       2517 CTCACTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCT 2576

Db     317398 CTGACCGATACCGACGTAGAGGAATACTACCACGGCTTCGCCAACCGCGTTCTCTGGCCG 317457

Qy       2577 CTTTTCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGG 2636

Db     317458 ATTTGCCACTACCGCCTTGATCTCGCCGAATACGGTCGCAAGGAAATGGCCGGGTATTTC 317517

Qy       2637 GAAGTAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTG 2696

Db     317518 CGCGTCAACCGCTTCTTCGCCCATCGCCTGGCGCCGCTTGTCAAACCCGATGACGTCATT 317577

Qy       2697 TGGGTGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGAT 2756

Db     317578 TGGGTGCACGACTACCCCTTGATTCCTCTCGCCGCGGAACTGCGTCAGATGGGCCTGGAG 317637

Qy       2757 TTGAAGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTG 2816

Db     317638 AACCGCATCGGCTTCTTCCTCCACATTCCCTGGCCGCCTGCAGACGTACTCTTCACGATG 317697

Qy       2817 C 2817

Db     317698 C 317698


RESULT 8
US-08-569-150A-2
; Sequence 2, Application US/08569150A
; Patent No. 5925804
;  GENERAL INFORMATION:
;    APPLICANT:  Hoekema, Andreas
;    APPLICANT:  Pen, Jan
;    APPLICANT:  Does, Mirjam P
;    APPLICANT:  Van Den Elzen, Petrus J. M
;    TITLE OF INVENTION:  PRODUCTION OF TREHALOSE IN PLANTS
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ladas & Parry
;      STREET:  26 West 61st Street
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10023
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3 1/4" disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  WordPerfect for Windows
;      SOFTWARE:  WordPerfect 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/569,150A
;      FILING DATE:  21-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP/94/02167
;      FILING DATE:  30-JUNE-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mass, Clifford J.
;      REGISTRATION NUMBER:  30,086
;      REFERENCE/DOCKET NUMBER:  U-010552-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 708-1890
;      TELEFAX:  (212) 246-8959
;      TELEX:  No. 5925804e
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1446 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Escherichia coli
;    IMMEDIATE SOURCE:
;      CLONE:  7F11
;    POSITION IN GENOME:
;      MAP POSITION:  41-42'
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..1446
;      OTHER INFORMATION:  /product= "trehalose phosphate synthase"
;      OTHER INFORMATION:  /gene= "otsA"
US-08-569-150A-2

  Query Match             2.5%;  Score 71.6;  DB 2;  Length 1446;
  Best Local Similarity   49.1%;  Pred. No. 1.4e-12;
  Matches  222;  Conservative    0;  Mismatches  224;  Indels    6;  Gaps    1;

Qy       2372 CTCCCCCAGCCCCGGTGGCCTTGTCACGGGGCTTTCCCCCGTTCTGGAACAACATCGTGG 2431

Db         75 CGCCGCCAGTGCCGGTGGCCTTGCCGTTGGCATACTGGGGGCACTGAAAGCCGCAGGCGG 134

Qy       2432 ATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAACAGATAC 2491

Db        135 ACTGTGGTTTGGCTGGAGTGGTGAAACAGGGAATGAGGATCAGCCGCTAAAAAAGGTGAA 194
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Qy       2492 GGGTG------TTTTGCTGCACCCTGTTGTCCTCACTGCAAGTGACTATGAAGGCTTCTA 2545
Db        195 AAAAGGTAACATTACGTGGGCCTCTTTTAACCTCAGCGAACAGGACCTTGACGAATACTA 254

Qy       2546 CGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACGATTTGATTGTTACTCCGGT 2605
Db        255 CAACCAATTCTCCAATGCCGTTCTCTGGCCCGCTTTTCATTATCGGCTCGATCTGGTGCA 314

Qy       2606 GTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCAAGTTCGCTGAAGCCGT 2665
Db        315 ATTTCAGCGTCCTGCCTGGGACGGCTATCTACGCGTAAATGCGTTGCTGGCAGATAAATT 374

Qy       2666 GAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGACTATCAGCTGTTGCTGGT 2725
Db        375 ACTGCCGCTGTTGCAAGACGATGACATTATCTGGATCCACGATTATCACCTGTTGCCATT 434

Qy       2726 TCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTTCTTCCTCCACATTCC 2785
Db        435 TGCGCATGAATTACGCAAACGGGGAGTGAATAATCGCATTGGTTTCTTTCTGCATATTCC 494

Qy       2786 CTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db        495 TTTCCCGACACCGGAAATCTTCAACGCGCTGC 526
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RESULT 9
US-08-274-121B-1
; Sequence 1, Application US/08274121B
; Patent No. 6133034
;  GENERAL INFORMATION:
;    APPLICANT:  Arne Reidar Strom
;    APPLICANT:  Inga Kaasen
;    APPLICANT:  Olaf Bay Styrvold
;    APPLICANT:  John McDougall
;    TITLE OF INVENTION:  Methods and Compositions
;    TITLE OF INVENTION:  Related To The Production
;    TITLE OF INVENTION:  of Trehalose
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 2.0 MB
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1(a)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/274,121B
;      FILING DATE:  12-JULY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/893,099
;      FILING DATE:  27-MAY-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 86(1)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (916) 753-6313
;      TELEFAX:  (916) 753-1510
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2868 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-274-121B-1

  Query Match             2.5%;  Score 71.6;  DB 3;  Length 2868;
  Best Local Similarity   49.1%;  Pred. No. 2.4e-12;
  Matches  222;  Conservative    0;  Mismatches  224;  Indels    6;  Gaps    1;

Qy       2372 CTCCCCCAGCCCCGGTGGCCTTGTCACGGGGCTTTCCCCCGTTCTGGAACAACATCGTGG 2431
Db       1500 CGCCGCCAGTGCCGGTGGCCTTGCCGTTGGCATACTGGGGGCACTGAAAGCCGCAGGCGG 1559

Qy       2432 ATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAACAGATAC 2491
Db       1560 ACTGTGGTTTGGCTGGAGTGGTGAAACAGGGAATGAGGATCAGCCGCTAAAAAAGGTGAA 1619

Qy       2492 GGGTG------TTTTGCTGCACCCTGTTGTCCTCACTGCAAGTGACTATGAAGGCTTCTA 2545
Db       1620 AAAAGGTAACATTACGTGGGCCTCTTTTAACCTCAGCGAACAGGACCTTGACGAATACTA 1679

Qy       2546 CGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACGATTTGATTGTTACTCCGGT 2605
Db       1680 CAACCAATTCTCCAATGCCGTTCTCTGGCCCGCTTTTCATTATCGGCTCGATCTGGTGCA 1739

Qy       2606 GTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCAAGTTCGCTGAAGCCGT 2665
Db       1740 ATTTCAGCGTCCTGCCTGGGACGGCTATCTACGCGTAAATGCGTTGCTGGCAGATAAATT 1799

Qy       2666 GAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGACTATCAGCTGTTGCTGGT 2725
Db       1800 ACTGCCGCTGTTGCAAGACGATGACATTATCTGGATCCACGATTATCACCTGTTGCCATT 1859

Qy       2726 TCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTTCTTCCTCCACATTCC 2785
Db       1860 TGCGCATGAATTACGCAAACGGGGAGTGAATAATCGCATTGGTTTCTTTCTGCATATTCC 1919

Qy       2786 CTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db       1920 TTTCCCGACACCGGAAATCTTCAACGCGCTGC 1951
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RESULT 10
US-09-489-039A-7037
; Sequence 7037, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 7037
;   LENGTH: 1479
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7037

  Query Match             2.5%;  Score 70.2;  DB 4;  Length 1479;
  Best Local Similarity   52.6%;  Pred. No. 4.2e-12;
  Matches  153;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy       2516 CCTCACTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCC 2575
Db        255 CCTTAATGAACGGGACCATGATGAATACTACAACCAGTTCTCTAACGCCGTGCTGTGGCC 314

Qy       2576 TCTTTTCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCG 2635
Db        315 GGCTTTCCACTATCGCCTTGATCTGGTCAGCTTTCAGCGCGAAGCCTGGGAGGGATATCT 374
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Qy       2636 GGAAGTAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGT 2695
Db        375 GCGGGTTAACGCCATGCTGGCGGACAAGCTTCTGCCGCTGATTGAGCCAGACGATACGCT 434

Qy       2696 GTGGGTGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGA 2755
Db        435 GTGGATCCATGATTACCATCTTCTGCCCTTCGCCAGCGAGCTGCGCAAGCGCGGGGTGAA 494

Qy       2756 TTTGAAGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTT 2806
Db        495 CAATCGCATCGGGTTTTTCTTACATATTCCGTTCCCGACGCCGGAGATTTT 545


RESULT 11
US-09-328-352-595
; Sequence 595, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 595
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-595

  Query Match             2.0%;  Score 56;  DB 4;  Length 1455;
  Best Local Similarity   49.7%;  Pred. No. 2.1e-07;
  Matches  143;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy       2530 ACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACGATT 2589
Db        242 AATATGCACAGTACTACTGTGGTTTTGCCAATAAAGTATTATGGCCTGCCATGCATGATC 301

Qy       2590 TGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCA 2649
Db        302 GGGATGACCTGATCGAATATAATGCAGAAGAATATAATACCTACCAAAAGGTCAATCGTT 361

Qy       2650 AGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGACT 2709
Db        362 TATTTGCTGAAAAATTACAACAGATTGCTCAGCCTGATGATCTGATTTGGGTGCATGACT 421

Qy       2710 ATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTT 2769
Db        422 ATCACTTTTTCAGCGTAGCTCGTCATTGCCGTGAATTAGGTATGCAAAATAAAATCGGTT 481

Qy       2770 TCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db        482 TCTTTTTGCATATTCCTTTCGCAAGCTTAAATATCTGGCGCAAGATCC 529


RESULT 12
US-09-248-796A-3169
; Sequence 3169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3169
;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-3169

  Query Match             1.9%;  Score 54.8;  DB 4;  Length 2241;
  Best Local Similarity   58.6%;  Pred. No. 7.6e-07;
  Matches   95;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy       2649 AAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGAC 2708
Db        268 AAAATAGTGGAAACATACAACGACGTGAATGATGAAGAGACAACTGTATGGATTCATGAC 327

Qy       2709 TATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGT 2768
Db        328 TACCACTTGTTATTAGTTCCCAAGATGGTTCGCGACAAGTTGCCTAATGCAAAAATCGGG 387

Qy       2769 TTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGT 2810
Db        388 TTTTTCTTGCATGTGTCTTTCCCTTCTTCAGAAGTTTTCCGT 429


RESULT 13
US-09-614-221A-160
; Sequence 160, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
;  APPLICANT: Karunanandaa, Balasulojini
;  APPLICANT:  Yu, Jaehyuk
;  APPLICANT:  Kishore, Ganesh M.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;  TITLE OF INVENTION:  WITH STEROL SYNTHESIS AND METABOLISM
;  FILE REFERENCE: 16516.075
;  CURRENT APPLICATION NUMBER: US/09/614,221A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/142,981
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 160
;   LENGTH: 3165
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-160

  Query Match             1.9%;  Score 52.6;  DB 4;  Length 3165;
  Best Local Similarity   49.1%;  Pred. No. 5.4e-06;
  Matches  139;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy       2527 GTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACG 2586
Db       1157 GTGCTTATAAGAACTACGCCAAACAGATTTTATGGCCCACTCTACATTATCAAATTCCAG 1216

Qy       2587 ATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACC 2646
Db       1217 ATAATCCAAATTCAAAGGCTTTTGAAGACCATTCTTGGGACTACTATCAAAAAGTGAATC 1276

Qy       2647 TCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGG 2706
Db       1277 AAAAGTTTTCTGATAGGATAGTTTCCGTTTACAAACCTGGCGACACAATTTGGATCCATG 1336

Qy       2707 ACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCG 2766
Db       1337 ATTATCATTTGATGCTTGTCCCACAAATGGTGAGAGAGAAACTGCCTAAAGCTAAGATTG 1396

Qy       2767 GTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCG 2809
Db       1397 GATTTTTCTTACACGTATCATTTCCAAGTAGTGAGGTCTTCAG 1439


RESULT 14
US-09-651-169A-36
; Sequence 36, Application US/09651169A
; Patent No. 6506565
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```
; GENERAL INFORMATION:
;  APPLICANT: Conner, Timothy W
;  APPLICANT:  Tzafrir, Iris
;  TITLE OF INVENTION: Plant Regulatory Sequences for Selective Control of Gene Expressi
;  FILE REFERENCE: 06009.0019.NPUS00  (RENN:019)
;  CURRENT APPLICATION NUMBER: US/09/651,169A
;  CURRENT FILING DATE:  2000-08-30
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
;   LENGTH: 654
;   TYPE: DNA
;   ORGANISM: Zea Mays
US-09-651-169A-36

  Query Match             1.7%;  Score 48;  DB 4;  Length 654;
  Best Local Similarity   51.4%;  Pred. No. 5.1e-05;
  Matches  108;  Conservative    1;  Mismatches  101;  Indels    0;  Gaps    0;

Qy       2608 ACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCAAGTTCGCTGAAGCCGTGA 2667
             ||  || || ||||  |       | |  |      ||  ||   ||||   | | |||
Db        359 ACCGCAGCGCTTGGGAGGCGTACGTGCTCGCCAACAAGTTCTTCTTCGAGAAGGTCGTCG 418

Qy       2668 GCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCAGGACTATCAGCTGTTGCTGGTTC 2727
             | |     |  | | || |   || ||||| || ||||| || ||  ||  | | |
Db        419 AGGTAATCAACCCGGAGGATGACTACGTTTGGGTTCACGACTACCATCTCATGGCGCTGC 478

Qy       2728 CTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTTCTTCCTCCACATTCCCT 2787
             ||  | |  | ||||       |       |    ||||| |||||||||||||: ||||
Db        479 CTACCTTCCTCCGCCGCTGCTTCAACCGCCTCCGCATCGGATTCTTCCTCCACAKCCCCT 538

Qy       2788 TCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
             |||| ||  | ||  | | |||    || |
Db        539 TCCCCTCGTCCGAGATCTACCGCACCCTCC 568


RESULT 15
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.7%;  Score 47.6;  DB 1;  Length 7218;
  Best Local Similarity   3.6%;  Pred. No. 0.00048;
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Job time : 262.002 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2817	100.0	2817	9	US-09-963-521-1	Sequence 1, Appli
3	2817	100.0	2817	9	US-09-834-721-1	Sequence 1, Appli
4	2817	100.0	2817	9	US-09-783-388-1	Sequence 1, Appli
5	2817	100.0	2817	10	US-09-951-535-1	Sequence 1, Appli
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7	2783.4	98.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
8	1836.6	65.2	1909	9	US-09-951-536-3	Sequence 3, Appli
9	1836.6	65.2	1909	9	US-09-963-521-3	Sequence 3, Appli
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13	1836.6	65.2	1909	17	US-10-224-574-11	Sequence 11, Appl
14	1561.2	55.4	1590	16	US-10-627-476-557	Sequence 557, App
15	1561.2	55.4	1590	16	US-10-450-055-41	Sequence 41, Appl
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22	327	11.6	327	9	US-09-738-626-2885	Sequence 2885, Ap
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45	66.2	2.4	1389	15	US-10-156-761-3920	Sequence 3920, Ap

ALIGNMENTS

RESULT 1
US-09-951-536-1
; Sequence 1, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-951-536-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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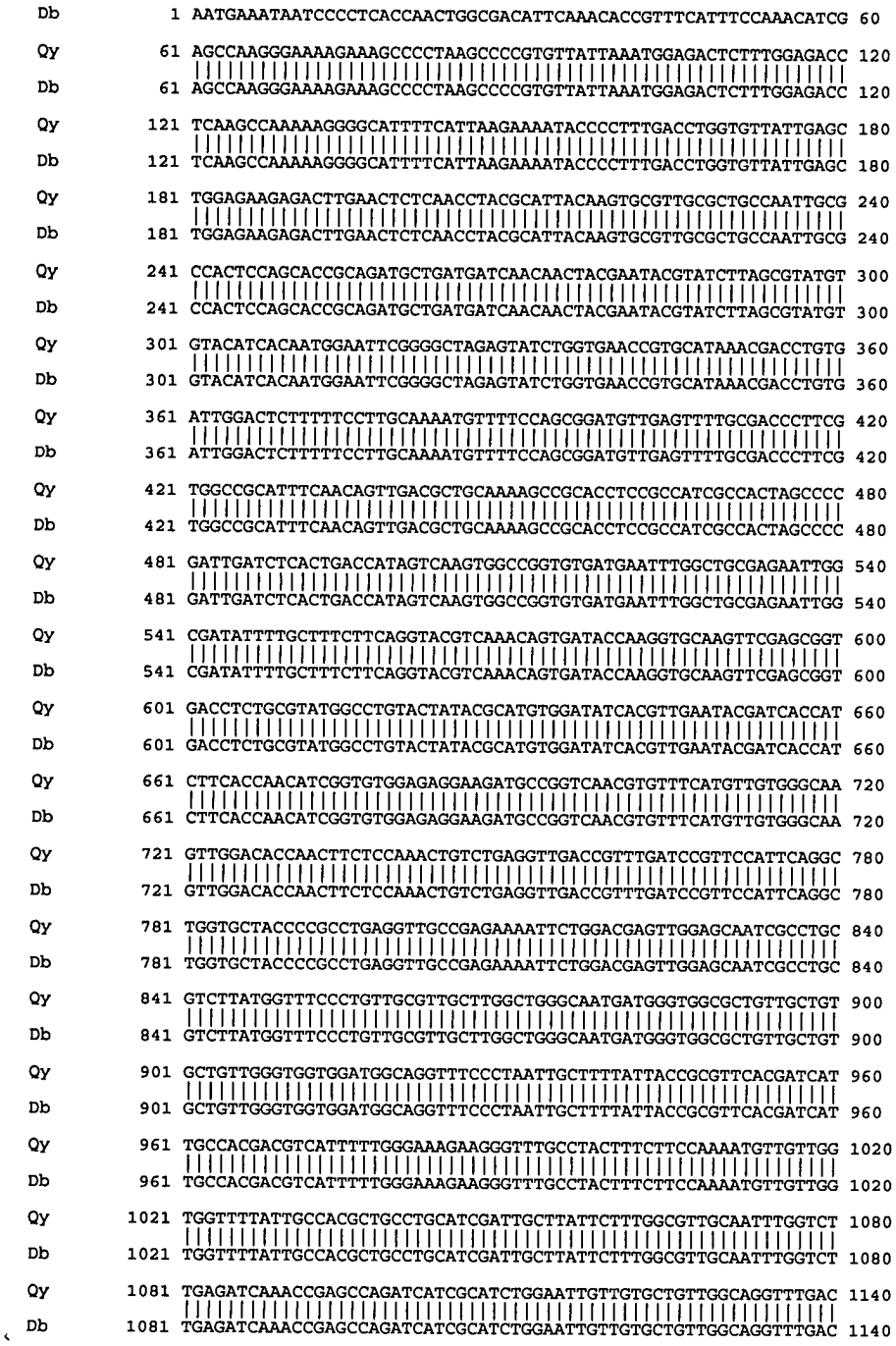
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RESULT 2
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; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-963-521-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240

Qy        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
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Qy        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
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Db        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360

Qy        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420

Qy        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480

Qy        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540
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Db        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540

Qy        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600
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Db        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600

Qy        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
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Qy        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780
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Qy        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840
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Qy        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
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Qy       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
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Db       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140

Qy       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200

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Qy       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
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Db       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740

Qy       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
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Db       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980

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Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
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Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
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Db       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340

Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
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Db       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400

Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
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Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460

Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
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Db       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520

Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
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RESULT 3
US-09-834-721-1
; Sequence 1, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE gene
US-09-834-721-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
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Db        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

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Db       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380

Qy       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
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Qy       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
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Qy       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
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Db       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620

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Db       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800

Qy       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860

Qy       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920

Qy       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980

Qy       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040

Qy       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100

Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220

Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280

Qy       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340

Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400

Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460

Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520

Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580

Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640

Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700

Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760

Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 4
US-09-783-388-1
; Sequence 1, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
US-09-783-388-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60

Qy         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120

Qy        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180

Qy        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240

Qy        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

Qy        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360

Qy        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420

Qy        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480

Qy        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540

Qy        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600

Qy        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660

Qy        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720

Qy        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780

Qy        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840

Qy        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
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Db        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900

Qy        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960

Qy        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020

Qy       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080

Qy       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140

Qy       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200

Qy       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260

Qy       1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320
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Db       1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320

Qy       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
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Db       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380

Qy       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440

Qy       1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500
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Db       1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500

Qy       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560

Qy       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
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Db       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620

Qy       1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680

Qy       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740

Qy       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800

Qy       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860

Qy       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920

Qy       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
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Db       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980

Qy       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040

Qy       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100

Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Db       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160

Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220

Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280

Qy       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340

Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400

Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460

Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520

Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580

Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
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Db       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640

Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
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Db       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700

Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760

Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 5
US-09-951-535-1
; Sequence 1, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT:  EGGELING, LOTHAR
;  APPLICANT:  SAHM, HERMANN
;  APPLICANT:  THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282415/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,535
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: DE 199 41 478.5
;  PRIOR FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
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; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-951-535-1

Query Match 100.0%; Score 2817; DB 10; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
Db    1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60

Qy   61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
Db   61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120

Qy  121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
Db  121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180

Qy  181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
Db  181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240

Qy  241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
Db  241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

Qy  301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
Db  301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360

Qy  361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
Db  361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420

Qy  421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480
Db  421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480

Qy  481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540
Db  481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540

Qy  541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600
Db  541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600

Qy  601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660
Db  601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660

Qy  661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
Db  661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720

Qy  721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780
Db  721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780

Qy  781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840
Db  781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840

Qy  841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
Db  841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900

Qy  901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
Db  901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960

Qy  961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
Db  961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020

Qy 1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
Db 1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080

Qy 1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
Db 1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140

Qy 1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
Db 1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200

Qy 1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
Db 1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260

Qy 1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320
Db 1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320

Qy 1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
Db 1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380

Qy 1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
Db 1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440

Qy 1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500
Db 1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500

Qy 1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
Db 1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560

Qy 1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
Db 1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620

Qy 1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680
Db 1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680

Qy 1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
Db 1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740

Qy 1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
Db 1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800

Qy 1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
Db 1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860

Qy 1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
Db 1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920

Qy 1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
Db 1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980

Qy 1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
Db 1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040

Qy 2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
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Db       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100

Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Db       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160

Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220

Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280

Qy       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340

Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400

Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460

Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520

Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580

Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640

Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700

Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760

Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 6
US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
;  APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
;  APPLICANT:  P. Peters- Wendisch
;  TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
;  TITLE OF INVENTION:  L-Serin, improved process for the microbial manufacture of L-ser
;  TITLE OF INVENTION:  genetically modified microorganism suitable for the process.
;  FILE REFERENCE: FZJ-9912-PCT
;  CURRENT APPLICATION NUMBER: US/10/224,574
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: C. glutamicum ATCC 14 752
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (398)..(1867)
;   OTHER INFORMATION: thr E  (Threonin-exportcarrier)
US-10-224-574-9

  Query Match           100.0%;  Score 2817;  DB 17;  Length 2817;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2817;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60

Qy         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120

Qy        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180

Qy        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240

Qy        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

Qy        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360

Qy        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420

Qy        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480

Qy        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540

Qy        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600

Qy        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660

Qy        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720

Qy        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780

Qy        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840

Qy        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900

Qy        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960

Qy        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
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Db        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
Qy       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
Db       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
Qy       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
Db       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
Qy       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
Db       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
Qy       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
Db       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
Qy       1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320
Db       1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320
Qy       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
Db       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
Qy       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
Db       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
Qy       1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500
Db       1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500
Qy       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
Db       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
Qy       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
Db       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
Qy       1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680
Db       1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680
Qy       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
Db       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
Qy       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
Db       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
Qy       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
Db       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
Qy       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
Db       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
Qy       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
Db       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
Qy       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
Db       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
Qy       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
Db       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
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Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
Db       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
Db       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
Db       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
Qy       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
Db       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
Db       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
Db       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
Db       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
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Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
Db       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
Db       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
Db       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
Db       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 7
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

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;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

  Query Match             98.8%;  Score 2783.4;  DB 9;  Length 3309400;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 2796;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 60
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Db    2790585 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG 2790644

Qy         61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
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Db    2790645 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCCGTGTTATTAAATGGAGACTTTTTGGAGACC 2790704

Qy        121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790705 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 2790764

Qy        181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790765 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 2790824

Qy        241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
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Qy        301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790885 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG 2790944

Qy        361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790945 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 2791004

Qy        421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791005 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC 2791064

Qy        481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791065 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATTGG 2791124

Qy        541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT 600
              |||||||||||||||||||||||||||||| ||||| |||||||| |||||||||||  ||
Db    2791125 CGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCAGT 2791184

Qy        601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT 660
              |||||||||||| ||  |||||||| |||||  ||||||||||||||||||||||||||||
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Qy        661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
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Qy        721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 780
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Db    2791305 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAGGC 2791364

Qy        781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCCTGC 840
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Db    2791365 TGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCTGC 2791424

Qy        841 GTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
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Qy        901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
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Qy        961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
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Qy       1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
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Qy       1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
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Db    2791665 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 2791724

Qy       1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db    2791725 ACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 2791784

Qy       1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT 1260
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Qy       1261 TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTATTC 1320
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Qy       1321 GTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
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Qy       1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 1440
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Db    2791965 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT 2792024

Qy       1441 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 1500
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Db    2792025 TTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGC 2792084

Qy       1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC 1560
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Qy       1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
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Db    2792145 GATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC 2792204

Qy       1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 1680
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Db    2792205 CCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTC 2792264

Qy       1681 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792265 ATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 2792324

Qy       1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
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Qy       1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
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Db    2792385 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAATAA 2792444

Qy       1861 AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
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Qy       1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
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Db    2792505 TCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 2792564
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Qy       1981 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2040
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Db    2792565 CAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGTGCCCGCAGGATTGTTGCCA 2792624

Qy       2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
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Qy       2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Qy       2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA 2220
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Qy       2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2280
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Db    2792805 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAAGAAGTCTTAAGCCG 2792864

Qy       2281 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792865 GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2792924

Qy       2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792925 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGGTGGCCTTGTCACGG 2792984

Qy       2401 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
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Db    2792985 GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2793044

Qy       2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2793045 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCACCCTGTTGTCCTCA 2793104

Qy       2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2580
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Db    2793105 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTT 2793164

Qy       2581 TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG 2640
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy       2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG 2700
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Qy       2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGCGCCCTGATTTGA 2760
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Qy       2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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Db    2793345 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2793401
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RESULT 8
US-09-951-536-3
; Sequence 3, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT:  EGGELING, LOTHAR
;  APPLICANT:  SAHM, HERMANN
;  APPLICANT:  THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282414/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,536
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
US-09-951-536-3

  Query Match             65.2%;  Score 1836.6;  DB 9;  Length 1909;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
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Qy        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
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Db        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
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Db        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
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Db        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

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Db        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
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Db        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
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Qy        816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
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Db        758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817

Qy        936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
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Db        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Qy        996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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Qy       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
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Qy       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
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Db       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
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Db       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
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Qy       1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
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Db       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy       2016 GCCGGTG 2022
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Db       1898 GCCGGGG 1904
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RESULT 9
US-09-963-521-3
; Sequence 3, Application US/09963521
; Patent No. US20020146781A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT:  EGGELING, LOTHAR
;  APPLICANT:  SAHM, HERMANN
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
;  TITLE OF INVENTION:  AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
;  TITLE OF INVENTION:  L-THREONINE USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282413/MAS
;  CURRENT APPLICATION NUMBER: US/09/963,521
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: DE 199 41 478.5
;  PRIOR FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
US-09-963-521-3

  Query Match             65.2%;  Score 1836.6;  DB 9;  Length 1909;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
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Db         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Db        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
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Db        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
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Db        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
              | |||||||| |||||||||| ||||||||||||||| ||  ||||||| ||||| ||||
Db        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
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Db        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577

Qy        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
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Db        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Qy       756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
Db       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

Qy       816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
Db       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757

Qy       876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935
Db       758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817

Qy       936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
Db       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy       996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
Db       878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937

Qy      1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
Db       938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175
Db       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy      1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
Db      1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy      1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
Db      1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy      1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
Db      1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy      1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
Db      1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy      1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
Db      1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy      1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
Db      1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

Qy      1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
Db      1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy      1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
Db      1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy      1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715
Db      1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy      1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775
Db      1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy      1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835
Db      1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy      1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895
Db      1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy      1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
Db      1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy      1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015
Db      1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy      2016 GCCGGTG 2022
Db      1898 GCCGGGG 1904
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RESULT 10
US-09-834-721-3
; Sequence 3, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC13032
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrE gene
US-09-834-721-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy       156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
Db        38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy       216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
Db        98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy       276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
Db       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Qy       396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
Db       278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy       456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
Db       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy       516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
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Db        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

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Qy        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Db        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

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Db        878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937

Qy       1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115

Db        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy       1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Db        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Db       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Db       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Db       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

Db       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475

Db       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Db       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

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Db       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Db       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Db       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Db       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Db       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Db       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Db       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Db       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy       2016 GCCGGTG 2022

Db       1898 GCCGGGG 1904
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RESULT 11
US-09-783-388-3
; Sequence 3, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC13032
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
US-09-783-388-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy         156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Db          38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy         216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Db          98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy         276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Db         158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
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Qy       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Db       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

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Db       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy       516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
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Db       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy       576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
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Db       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy       636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
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Db       518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577

Qy       696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
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Db       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

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Db       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

Qy       816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
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Db       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757

Qy       876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935
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Db       758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817

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Db       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy       996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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Db       878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937

Qy      1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy      1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy      1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy      1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy      1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy      1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy      1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

Qy      1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy      1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy      1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy      1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy      1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy      1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895
            |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy      1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy      1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy      2016 GCCGGTG 2022
            ||||| |
Db      1898 GCCGGGG 1904
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RESULT 12
US-09-951-535-3
; Sequence 3, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrE-Gen

US-09-951-535-3

Query Match 65.2%; Score 1836.6; DB 10; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy       156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
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Db        38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy       216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy       276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy       396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy       456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy       516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy       576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
            | |||||||| |||||||||| |||||||||||||| ||  ||||||| ||||| ||||
Db       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy       636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577

Qy       696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy       756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |
Db       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

Qy       816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757

Qy       876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935
            |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817

Qy       936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy       996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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Db       878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937

Qy      1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy      1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy      1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy      1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy      1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy      1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy      1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

Qy      1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy      1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy      1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy      1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy      1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy      1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895
            |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy      1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy      1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Qy      2016 GCCGGTG 2022
            ||||| |
Db      1898 GCCGGGG 1904
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RESULT 13
US-10-224-574-11
; Sequence 11, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: FZJ-9912-PCT

```
;  CURRENT APPLICATION NUMBER: US/10/224,574
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: C. glutanicum ATCC 13 032
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thr E  (Threonin-exportcarrier)
US-10-224-574-11

  Query Match            65.2%;  Score 1836.6;  DB 17;  Length 1909;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy       216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy       276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy       396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy       456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy       516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy       576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
            | |||||||| |||||||||||| |||||||||||||| || |||||| ||||| ||||
Db       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy       636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577

Qy       696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy       756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |
Db       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

Qy       816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757

Qy       876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935
            |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817

Qy       936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy       996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937

Qy      1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057

Qy      1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy      1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy      1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy      1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy      1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357

Qy      1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417

Qy      1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy      1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537

Qy      1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597

Qy      1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657

Qy      1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717

Qy      1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895
            |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777

Qy      1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
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Db      1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

Qy      1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2016 GCCGGTG 2022
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RESULT 14
US-10-627-476-557
; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schoder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CPCN
;  CURRENT APPLICATION NUMBER: US/10/627,476
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 09/602,787
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
;   LENGTH: 1590
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1567)
;   OTHER INFORMATION: RXN00349
US-10-627-476-557

  Query Match             55.4%;  Score 1561.2;  DB 16;  Length 1590;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1572;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy        298 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 60

Qy        358 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 120

Qy        418 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 180

Qy        478 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 240

Qy        538 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy        598 GGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCAC 657
              ||||||||||||||| || ||||||| ||||| ||||||||||||||||||||||||||
Db        301 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 360

Qy        658 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGG 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        361 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG 420

Qy        718 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 480

Qy        778 GGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCC 837
              |||||||| |||||||||||||||||||||||||| |||||||||||||||||||| ||
Db        481 GGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCC 540

Qy        838 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGC 897
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGC 600

Qy        898 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 660

Qy        958 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy       1018 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 1077
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Db        721 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy       1078 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 840

Qy       1138 GACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACG 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1198 ATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 1257
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 960

Qy       1258 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1020

Qy       1318 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1080

Qy       1378 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1140

Qy       1438 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1200

Qy       1498 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1260

Qy       1558 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1320

Qy       1618 CACCTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1677
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1738 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1797

Db       1441 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1500

Qy       1798 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAA 1857

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; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
;  APPLICANT: BASF Aktiengesellschaft
;  TITLE OF INVENTION: No. US20040043953A1el genes of Corynebacterium
;  FILE REFERENCE: 936_2000
;  CURRENT APPLICATION NUMBER: US/10/450,055
;  CURRENT FILING DATE:  2003-06-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
;   LENGTH: 1590
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1567)
;   OTHER INFORMATION: RXS00349
US-10-450-055-41

  Query Match           55.4%;  Score 1561.2;  DB 16;  Length 1590;
  Best Local Similarity  98.9%;  Pred. No. 0;
  Matches 1572;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy        298 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 357

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Qy        358 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 417

Db         61 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 120

Qy        418 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 477

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Qy        598 GGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCAC 657

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Qy        658 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGG 717

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Qy        838 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGC 897

Db        541 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGC 600

Qy        898 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 957

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Qy        958 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 1017

Db        661 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy       1018 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 1077

Db        721 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy       1078 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 1137

Db        781 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 840

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Qy       1258 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1317

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Qy       1438 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1497

Db       1141 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1200

Qy       1498 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1557

Db       1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1260

Qy       1558 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1617

Db       1261 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1320

Qy       1618 CACCTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1677

Db       1321 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1380

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Qy       1738 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1797

Db       1441 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1500

Qy       1798 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAA 1857

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Qy       1858 TAAAAGGTAAAAATCAACCTGCTTAGGCGT 1887
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Job time : 1549.15 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 08:54:47 ; Search time 163.998 Seconds
(without alignments)
8273.863 Million cell updates/sec

Title: US-09-963-521-3
Perfect score: 1909
Sequence: 1 agcttgcatgcctgcaggtc.....aaaccgcagccggggtaccg 1909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1909	100.0	1909	4	US-09-431-099-3	Sequence 3, Appli
	2	1836.6	96.2	2817	4	US-09-431-099-1	Sequence 1, Appli
	3	1590	83.3	1590	4	US-09-602-787A-557	Sequence 557, App
	4	86.6	4.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	5	86.6	4.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	6	47.6	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl
c	7	46.6	2.4	400	4	US-08-956-171E-4234	Sequence 4234, Ap
c	8	46.6	2.4	400	4	US-08-781-986A-4234	Sequence 4234, Ap
	9	45.8	2.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	10	45.6	2.4	381	4	US-08-956-171E-4023	Sequence 4023, Ap
	11	45.6	2.4	381	4	US-08-781-986A-4023	Sequence 4023, Ap
	12	44.4	2.3	237	4	US-08-956-171E-4566	Sequence 4566, Ap
	13	44.4	2.3	237	4	US-08-781-986A-4566	Sequence 4566, Ap
	14	44.4	2.3	239	4	US-08-956-171E-4543	Sequence 4543, Ap
	15	44.4	2.3	239	4	US-08-956-171E-4544	Sequence 4544, Ap
	16	44.4	2.3	239	4	US-08-781-986A-4543	Sequence 4543, Ap
	17	44.4	2.3	239	4	US-08-781-986A-4544	Sequence 4544, Ap
	18	44.4	2.3	400	4	US-08-956-171E-3631	Sequence 3631, Ap
	19	44.4	2.3	400	4	US-08-956-171E-3660	Sequence 3660, Ap
	20	44.4	2.3	400	4	US-08-956-171E-4198	Sequence 4198, Ap
	21	44.4	2.3	400	4	US-08-781-986A-3631	Sequence 3631, Ap
	22	44.4	2.3	400	4	US-08-781-986A-3660	Sequence 3660, Ap
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	25	44.4	2.3	411	4	US-08-781-986A-4353	Sequence 4353, Ap
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	28	44.4	2.3	6591	4	US-08-956-171E-3114	Sequence 3114, Ap
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c	30	43.4	2.3	400	4	US-08-956-171E-3542	Sequence 3542, Ap
c	31	43.4	2.3	400	4	US-08-956-171E-3723	Sequence 3723, Ap
c	32	43.4	2.3	400	4	US-08-781-986A-3542	Sequence 3542, Ap
c	33	43.4	2.3	400	4	US-08-781-986A-3723	Sequence 3723, Ap
c	34	43.4	2.3	1171	4	US-08-956-171E-3539	Sequence 3539, Ap
c	35	43.4	2.3	1171	4	US-08-781-986A-3539	Sequence 3539, Ap
	36	43.4	2.3	3189	4	US-09-710-279-3694	Sequence 3694, Ap
	37	43.4	2.3	3305	4	US-09-710-279-4156	Sequence 4156, Ap
	38	42	2.2	339	4	US-08-956-171E-4263	Sequence 4263, Ap
	39	42	2.2	339	4	US-08-781-986A-4263	Sequence 4263, Ap
	40	41.8	2.2	2869	4	US-09-710-279-4402	Sequence 4402, Ap
	41	41.8	2.2	3012	4	US-09-710-279-3707	Sequence 3707, Ap
	42	41.8	2.2	3232	4	US-09-710-279-4217	Sequence 4217, Ap
	43	41.2	2.2	400	4	US-08-956-171E-4029	Sequence 4029, Ap
	44	41.2	2.2	400	4	US-08-781-986A-4029	Sequence 4029, Ap
	45	40	2.1	2870	5	PCT-US93-07213-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-431-099-3
; Sequence 3, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT: Degussa-HOls AG
; APPLICANT: Forschungszentrum-JOlich GmbH
; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC13032
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrE-Gen
US-09-431-099-3

Query Match 100.0%; Score 1909; DB 4; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCTTTGACCTGGTGTTATTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCTTTGACCTGGTGTTATTGA 60

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120

Qy        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Qy        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240

Qy        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300

Qy        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
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Db        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
Qy        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
Db        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
Qy        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
Db        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
Qy        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
Db        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
Qy        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
Db        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
Qy        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
Db        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
Qy        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
Db        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
Qy        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780
Db        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780
Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
Db        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
Qy        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
Db        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
Qy        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
Db        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
Qy        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
Db        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
Qy       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
Db       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
Qy       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
Db       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
Db       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
Db       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
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Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
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RESULT 2
US-09-431-099-1
; Sequence 1, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT: Degussa-HOls AG
; APPLICANT: Forschungszentrum-JOlich GmbH
; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-431-099-1

Query Match 96.2%; Score 1836.6; DB 4; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
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Qy       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
Db       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy       278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
Db       396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
Db       456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
Db       516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
Db       576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

Qy       518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
Db       636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
Db       696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
Db       756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

Qy       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
Db       816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875

Qy       758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817
Db       876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935

Qy       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
Db       936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995

Qy       878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937
Db       996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055

Qy       938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
Db      1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115

Qy       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
Db      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Qy      1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
Db      1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Qy      1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
Db      1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy      1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
Db      1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Qy      1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
Db      1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

Qy      1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357
Db      1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475

Qy      1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
Db      1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Qy      1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
Db      1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595

Qy      1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
Db      1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy      1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
Db      1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Qy      1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
Db      1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy      1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
Db      1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Qy      1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
Db      1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Qy      1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
Db      1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy      1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
Db      1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy      1898 GCCGGGG 1904
Db      2016 GCCGGTG 2022
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RESULT 3
US-09-602-787A-557
; Sequence 557, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr"ger, Burkhard
; APPLICANT: Sch"der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
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; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
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; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-09-602-787A-557

Query Match 83.3%; Score 1590; DB 4; Length 1590;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      180 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 239
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Db        1 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 60

Qy      240 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 299
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Db       61 GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT 120

Qy      300 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 180

Qy      360 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAAT 240

Qy      420 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy      480 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 360

Qy      540 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG 599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG 420

Qy      600 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 659
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 480

Qy      660 GGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCC 719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCC 540

Qy      720 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGC 779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGC 600

Qy      780 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 839
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 660

Qy      840 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 899
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy      900 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy      960 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 1019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTT 840

Qy     1020 GACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACG 1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACG 900

Qy     1080 ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 1139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCA 960

Qy     1140 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTA 1020

Qy     1200 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 TTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGG 1080

Qy     1260 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1319
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Db       1081 TTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGC 1140

Qy       1320 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1379

Db       1141 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1200

Qy       1380 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1439

Db       1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGT 1260

Qy       1440 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1499

Db       1261 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1320

Qy       1500 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1559

Db       1321 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1380

Qy       1560 TTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1619

Db       1381 TTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1440

Qy       1620 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1679

Db       1441 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1500

Qy       1680 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAA 1739

Db       1501 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAA 1560

Qy       1740 TAAAAGGTAAAAATCAACCTGCTTAGGCGT 1769

Db       1561 TAAAAGGTAAAAATCAACCTGCTTAGGCGT 1590
```

RESULT 4
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 4.5%; Score 86.6; DB 3; Length 4403765;
Best Local Similarity 45.6%; Pred. No. 1.3e-14;
Matches 498; Conservative 0; Mismatches 559; Indels 36; Gaps 4;

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Qy        531 TACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCA 590

Db    4180213 TACCACCATCATCGTGTCCGCGCTAGCGACCACAGACACTCCGCCGGTCACCATCATGCG 4180272

Qy        591 TGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCG 650

Db    4180273 GTCGGTCCGGACCCGGTCCACTGACTACAGCCGGCTGGCCGAACTCGATCGACTCGTTCA 4180332

Qy        651 TTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGA 710

Db    4180333 GCGGATAACCTCCGGTGGCGTCGCAGTCGACCAGGCTCACGAGGCTATGGACGAGTTGAC 4180392

Qy        711 GCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGG 770

Db    4180393 CGAACGGCCCCACCCCTACCCGCGCTGGCTCGCGACCGCGGGGGCGGCGGGCTTCGCACT 4180452

Qy        771 TGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGC 830

Db    4180453 CGGCGTCGCCATGTTGCTCGGCGGAACCTGGCTGACCTGCGTCTTGGCTGCCGTGACGTC 4180512

Qy        831 GTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCA 890

Db    4180513 TGGCGTGATCGACCGACTGGGCCGGCTGCTGAACCGGATCGGGACCCCGTTGTTCTTCCA 4180572

Qy        891 AAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTT 950

Db    4180573 GCGCGTGTTCGGCGCGGGGATCGCGACCCTGGTCGCGGTGGCGGCTTACCTGATCGCCGG 4180632

Qy        951 GCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTT 1010

Db    4180633 CCA---------------GGATCCGACCGCGCTGGTGGCCACCGGAATCGTTGTGCTGCT 4180677

Qy       1011 GGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGC 1070

Db    4180678 GTCTGGGATGACCTTGGTGGGTTCGATGCAGGACGCGGTCACCGGGTACATGCTCACCGC 4180737

Qy       1071 AAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGT------ 1124

Db    4180738 ACTCGCCCGGCTTGGCGACGCCCTGTTCCTGACCGCAGGGATCGTCGTCGGCATCCTCAT 4180797

Qy       1125 ---------GGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCAT 1175

Db    4180798 CTCGTTGCGGGGCGTCACCAATGCCGGCATCCAGATCGAACTGCATGTCGACGCAACCAC 4180857

Qy       1176 GGAGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGT 1235

Db    4180858 GACGCTCGCCACCCCGGGCATGCCGCTACCGATTCTCGTCGCGGTAAGCGGTGCGGCGCT 4180917

Qy       1236 CACCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGG 1295

Db    4180918 GTCCGGCGTGTGCCTGACGATCGCGAGCTATGCGCCGCTACGTTCTGTGGCCACCGCCGG 4180977

Qy       1296 GCTTACTGC---GCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCC 1352

Db    4180978 ACTCTCGGCCGGACTCGCCGAACTGGTGCTCATCGGACTCGGCGCGGCCGGGTTCGGCCG 4181037

Qy       1353 CGTCTCTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCG 1412

Db    4181038 AGTGGTCGCCACCTGGACCGCCGCGATCGGCGTCGGCTTCTTGGCCACCCTGATCTCAAT 4181097

Qy       1413 TCGATTCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGG 1472

Db    4181098 CCGTCGGCAGGCTCCCGCCTTGGTGACGGCCACCGCCGGCATCATGCCGATGCTGCCGGG 4181157

Qy       1473 TCTAGCAATTTACCGCGGAATGTACGC---CACCCTGAATGATCAAACACTCATGGGTTT 1529

Db    4181158 CCTTGCGGTCTTCCGTGCCGTGTTCGCGTTCGCCGTCAATGACACACCCGACGGCGGTCT 4181217

Qy       1530 CACCAACATTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGG 1589

Db    4181218 GACCCAGCTGCTGGAAGCGGCCGCGACTGCACTCGCGCTTGGCAGCGGGGTGGTGTTGGG 4181277

Qy       1590 TGAGTGGATTGCC 1602

Db    4181278 CGAGTTCCTCGCC 4181290
```

RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A

```
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             4.5%;  Score 86.6;  DB 3;  Length 4411529;
  Best Local Similarity   45.6%;  Pred. No. 1.3e-14;
  Matches  498;  Conservative    0;  Mismatches  559;  Indels   36;  Gaps    4;

Qy        531 TACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCA 590
              ||| | || |||| |  ||    | |           |    |||||||| | |  | ||
Db    4187965 TACCACCATCATCGTGTCCGCGCTAGCGACCACAGACACTCCGCCGGTCACCATCATGCG 4188024

Qy        591 TGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCG 650
              ||  | |    |  |||  ||| | |   ||| | ||  | || ||  | | ||
Db    4188025 GTCGGTCCGGACCCGGTCCACTGACTACAGCCGGCTGGCCGAACTCGATCGACTCGTTCA 4188084

Qy        651 TTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGA 710
              ||      | ||||    | |    ||   ||  |  |     ||||||||||
Db    4188085 GCGGATAACCTCCGGTGGCGTCGCAGTCGACCAGGCTCACGAGGCTATGGACGAGTTGAC 4188144

Qy        711 GCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGG 770
              ||   ||      | ||       |     | |||       ||   |||     | |
Db    4188145 CGAACGGCCCCACCCCTACCCGCGCTGGCTCGCGACCGCGGGGGCGGCGGGCTTCGCACT 4188204

Qy        771 TGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGC 830
              |  || ||  || || | || ||    |||| |   | | |  | |||     | ||  |
Db    4188205 CGGCGTCGCCATGTTGCTCGGCGGAACCTGGCTGACCTGCGTCTTGGCTGCCGTGACGTC 4188264

Qy        831 GTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCA 890
              |  ||||      |      |  ||    ||  ||    ||    ||||||||
Db    4188265 TGGCGTGATCGACCGACTGGGCCGGCTGCTGAACCGGATCGGGACCCCGTTGTTCTTCCA 4188324

Qy        891 AAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTT 950
              ||  | || |     || || || |||   ||    |  |||||     | ||
Db    4188325 GCGCGTGTTCGGCGCGGGGATCGCGACCCTGGTCGCGGTGGCGGCTTACCTGATCGCCGG 4188384

Qy        951 GCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTT 1010
              ||                | |||| |  | |  | ||  | ||||| |||||||| |
Db    4188385 CCA---------------GGATCCGACCGCGCTGGTGGCCACCGGAATCGTTGTGCTGCT 4188429

Qy       1011 GGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGC 1070
              | | ||  ||||  | |||   ||  |||||||||   ||||  ||      | | || ||
Db    4188430 GTCTGGGATGACCTTGGTGGGTTCGATGCAGGACGCGGTCACCGGGTACATGCTCACCGC 4188489

Qy       1071 AAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGT------ 1124
              |   || ||  ||  |||  | ||  |  | ||||  || || || |   ||| |
Db    4188490 ACTCGCCCGGCTTGGCGACGCCCTGTTCCTGACCGCAGGGATCGTCGTCGGCATCCTCAT 4188549

Qy       1125 ---------GGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCAT 1175
                      |||  |   || |          | |||   |       |      |  |||
Db    4188550 CTCGTTGCGGGGCGTCACCAATGCCGGCATCCAGATCGAACTGCATGTCGACGCAACCAC 4188609

Qy       1176 GGAGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGT 1235
              |  | |||  |  |   |          | |   ||| |   | | ||  ||   |   |
Db    4188610 GACGCTCGCCACCCCGGGCATGCCGCTACCGATTCTCGTCGCGGTAAGCGGTGCGGCGCT 4188669

Qy       1236 CACCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGG 1295
                  |||  | |  | |  |  | |   | || |||  |       || |||   |  || ||
Db    4188670 GTCCGGCGTGTGCCTGACGATCGCGAGCTATGCGCCGCTACGTTCTGTGGCCACCGCCGG 4188729

Qy       1296 GCTTACTGC---GCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCC 1352
                ||  | ||    ||    |      | | |        |||  ||  |    || ||||
Db    4188730 ACTCTCGGCCGGACTCGCCGAACTGGTGCTCATCGGACTCGGCGCGGCCGGGTTCGGCCG 4188789

Qy       1353 CGTCTCTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCG 1412
                ||    ||| |   ||  || || |   |  || || |||    |       || |  |
Db    4188790 AGTGGTCGCCACCTGGACCGCCGCGATCGGCGTCGGCTTCTTGGCCACCCTGATCTCAAT 4188849

Qy       1413 TCGATTCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGG 1472
                ||       |  |||  | |||  |   ||| |  ||||||||||  || ||||| || ||
Db    4188850 CCGTCGGCAGGCTCCCGCCTTGGTGACGGCCACCGCCGGCATCATGCCGATGCTGCCGGG 4188909

Qy       1473 TCTAGCAATTTACCGCGGAATGTACGC---CACCCTGAATGATCAAACACTCATGGGTTT 1529
                || ||  | | ||| |   ||| |||    | || | |||||    | |   |   ||| |
Db    4188910 CCTTGCGGTCTTCCGTGCCGTGTTCGCGTTCGCCGTCAATGACACACCCGACGGCGGTCT 4188969

Qy       1530 CACCAACATTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGG 1589
                |||  |   ||  ||    || |||||     | |||| |   ||  ||||| |||||
Db    4188970 GACCCAGCTGCTGGAAGCGGCCGCGACTGCACTCGCGCTTGGCAGCGGGGTGGTGTTGGG 4189029

Qy       1590 TGAGTGGATTGCC 1602
                ||||   | |||
Db    4189030 CGAGTTCCTCGCC 4189042


RESULT 6
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.5%;  Score 47.6;  DB 1;  Length 7218;
  Best Local Similarity   3.6%;  Pred. No. 0.00059;
  Matches   14;  Conservative  218;  Mismatches  162;  Indels    0;  Gaps    0;

Qy       1057 GCTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTT 1116
              ||| | |    ||  ||    ||||:::::    : ::::: ::: ::  :  : :: ::
Db       1042 GCTGCAGGTCGAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1101

Qy       1117 GCTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATG 1176
              ::  : :   :::   : :::  ::::::    :::: : : :: : :: ::: :: :
Db       1102 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1161

Qy       1177 GAGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTC 1236
                ::: :: :  : :::  :: ::: ::: : ::: ::: : :: :: ::  :  : ::
Db       1162 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1221

Qy       1237 ACCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGG 1296
              :: :  :  ::::: :  :   :: :: : :    :  :::::  :  :: :: :
Db       1222 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1281

Qy       1297 CTTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTC 1356
              ::: :: : ::  :   :::: : :::: :: :::::: :: ::: :::   :::: ::
Db       1282 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1341

Qy       1357 TCTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGA 1416
              ::: :: :: :  :: :: :  :  :  ::  :::: ::  :  ::: ::: ::: ::
Db       1342 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1401

Qy       1417 TTCTTGATTCCACCGTTGATTGTGGCGATTGCCG 1450
              :::::  :::: :: ::  :: :  :  :: ::|
Db       1402 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYG 1435


RESULT 7
US-08-956-171E-4234/c
; Sequence 4234, Application US/08956171E
; Patent No. 6593114
;  GENERAL INFORMATION:
;       APPLICANT: Charles Kunsch
;                  Gil H. Choi
;                  Patrick S. Dillon
;                  Craig A. Rosen
;                  Steven C. Barash
;                  Michael R. Fannon
;       TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;       NUMBER OF SEQUENCES: 5256
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;            COMPUTER: HP Vectra 486/33
;            OPERATING SYSTEM: MSDOS version 6.2
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/956,171E
;            FILING DATE: 20-Oct-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/009,861
;            FILING DATE: January 5, 1996
;            APPLICATION NUMBER: 08/781,986
;            FILING DATE: January 3, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mark J. Hyman
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB248P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (240) 314-1224
;            TELEFAX: (301) 309-8439
;  INFORMATION FOR SEQ ID NO: 4234:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 400 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4234:
US-08-956-171E-4234

  Query Match             2.4%;  Score 46.6;  DB 4;  Length 400;
  Best Local Similarity   61.9%;  Pred. No. 0.00022;
  Matches   73;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         32 ATCCCCCCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTAC 91
              | |||   | ||   |||       || | || ||  |   |||||||| | ||||||||
Db        298 AGCCCANTCGTTACCCCTCCATAAATGGTGCCGGCCAGAGGACTTGAACCCCCAACCTAC 239

Qy         92 GCATTACAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGA 149
                |||||||||  ||||| || ||||||| || |  || ||   | |   | | | ||
Db        238 TGATTACAAGTCAGTTGCTCTACCAATTGAGCTAGGCCGGCTAAGAAATGGTTCAGGA 181


RESULT 8
US-08-781-986A-4234/c
; Sequence 4234, Application US/08781986A
; Patent No. 6737248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  4234:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  400 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-4234

  Query Match             2.4%;  Score 46.6;  DB 4;  Length 400;
  Best Local Similarity   61.9%;  Pred. No. 0.00022;
  Matches   73;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;
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Qy          32 ATCCCCCCCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTAC 91
               |||    | ||   |||       || | || ||  |   |||||||||| | ||||||||
Db         298 AGCCCANTCGTTACCCCTCCATAAATGGTGCCGGCCAGAGGACTTGAACCCCCAACCTAC 239

Qy          92 GCATTACAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGA 149
               |||||||||  ||||| || ||||||| || |  || ||   | |   | | | ||
Db         238 TGATTACAAGTCAGTTGCTCTACCAATTGAGCTAGGCCGGCTAAGAAATGGTTCAGGA 181


RESULT 9
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (15001)..(30000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (30001)..(45000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (45001)..(60000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (60001)..(75000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
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;   LOCATION: (165001)..(180000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (180001)..(195000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   LOCATION: (210001)..(225000)
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;   LOCATION: (225001)..(240000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (240001)..(255000)
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;   NAME/KEY: misc_feature
;   LOCATION: (255001)..(270000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (270001)..(285000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (285001)..(300000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
;   LOCATION: (330001)..(345000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (345001)..(360000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   NAME/KEY: misc_feature
;   LOCATION: (375001)..(390000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (390001)..(405000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (405001)..(420000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (435001)..(450000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (450001)..(465000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
;   LOCATION: (480001)..(495000)
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;   LOCATION: (495001)..(510000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (510001)..(525000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (525001)..(540000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (540001)..(555000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (555001)..(570000)
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;   LOCATION: (570001)..(585000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (585001)..(600000)
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;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (600001)..(615000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (615001)..(630000)
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;   NAME/KEY: misc_feature
;   LOCATION: (630001)..(645000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (645001)..(660000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (660001)..(675000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (675001)..(690000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (690001)..(705000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
;   LOCATION: (720001)..(735000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (735001)..(750000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (750001)..(765000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (765001)..(780000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (780001)..(795000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (795001)..(810000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (810001)..(825000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (840001)..(855000)
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;   NAME/KEY: misc_feature
;   LOCATION: (855001)..(870000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (870001)..(885000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (885001)..(900000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (900001)..(915000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature

  Query Match             2.4%;  Score 45.8;  DB 4;  Length 1230025;
  Best Local Similarity   76.7%;  Pred. No. 0.046;
  Matches   56;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
              |||||||||  || ||||| |||||||     ||||||| |    ||| ||||||||||
Db     303710 GCTGGAGAAAGGAATTGAACCCTCAACCGTTCGATTACAAATCGAATGCTCTGCCAATTG 303769

Qy        121 CGCCACTCCAGCA 133
              || |||||||||
Db     303770 AGCTACTCCAGCA 303782


RESULT 10
US-08-956-171E-4023
; Sequence 4023, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 4023:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 381 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4023:
US-08-956-171E-4023

  Query Match             2.4%;  Score 45.6;  DB 4;  Length 381;
  Best Local Similarity   73.1%;  Pred. No. 0.00043;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
              || | || ||  |    ||||||||| | ||||||||  |||||||||  ||||| || ||
Db         87 ATGGNGCNGGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 146

Qy        116 AATTGCGCCACTCCAGCA 133
              ||||| || |  || |||
Db        147 AATTGAGCTAGGCCGGCA 164


RESULT 11
US-08-781-986A-4023
; Sequence 4023, Application US/08781986A
; Patent No. 6737248
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;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  4023:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  381 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-4023

  Query Match             2.4%;  Score 45.6;  DB 4;  Length 381;
  Best Local Similarity   73.1%;  Pred. No. 0.00043;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
              || | || ||  |   ||||||||| | ||||||||  |||||||||  ||||| || ||
Db         87 ATGGNGCNGGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 146

Qy        116 AATTGCGCCACTCCAGCA 133
              ||||| || |  || |||
Db        147 AATTGAGCTAGGCCGGCA 164


RESULT 12
US-08-956-171E-4566
; Sequence 4566, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 4566:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 237 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4566:
US-08-956-171E-4566

  Query Match             2.3%;  Score 44.4;  DB 4;  Length 237;
  Best Local Similarity   73.1%;  Pred. No. 0.00078;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
              || | || ||  |   ||||||||| | ||||||||  |||||||||  ||||| || ||
Db         25 ATGGTGCCGGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 84

Qy        116 AATTGCGCCACTCCAGCA 133
              ||||| || |  || |||
Db         85 AATTGAGCTAGGCCGGCA 102


RESULT 13
US-08-781-986A-4566
; Sequence 4566, Application US/08781986A
; Patent No. 6737248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  4566:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  237 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-4566

  Query Match             2.3%;  Score 44.4;  DB 4;  Length 237;
  Best Local Similarity   73.1%;  Pred. No. 0.00078;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
              || | || ||  |   ||||||||| | ||||||||  |||||||||  ||||| || ||
Db         25 ATGGTGCCGGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 84

Qy        116 AATTGCGCCACTCCAGCA 133
              ||||| || |  || |||
Db         85 AATTGAGCTAGGCCGGCA 102


RESULT 14
US-08-956-171E-4543
; Sequence 4543, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 4543:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 239 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4543:
US-08-956-171E-4543

  Query Match             2.3%;  Score 44.4;  DB 4;  Length 239;
  Best Local Similarity   73.1%;  Pred. No. 0.00079;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
              || | || ||  |   ||||||||| | ||||||||  |||||||||  ||||| || ||
Db         81 ATGGTGCCGGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 140

Qy        116 AATTGCGCCACTCCAGCA 133
              ||||| || |  || |||
Db        141 AATTGAGCTAGGCCGGCA 158


RESULT 15
US-08-956-171E-4544
; Sequence 4544, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 4544:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 239 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4544:
US-08-956-171E-4544

  Query Match             2.3%;  Score 44.4;  DB 4;  Length 239;
  Best Local Similarity   73.1%;  Pred. No. 0.00079;
  Matches   57;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

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Search completed: January 14, 2005, 10:08:58
Job time : 176.998 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 09:56:14 ; Search time 969.85 Seconds
(without alignments)
11309.899 Million cell updates/sec

Title: US-09-963-521-3
Perfect score: 1909
Sequence: 1 agcttgcatgcctgcaggtc.....aaaccgcagccggggtaccg 1909

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1909	100.0	1909	9	US-09-951-536-3	Sequence 3, Appli
2	1909	100.0	1909	9	US-09-963-521-3	Sequence 3, Appli
3	1909	100.0	1909	9	US-09-834-721-3	Sequence 3, Appli
4	1909	100.0	1909	9	US-09-783-388-3	Sequence 3, Appli
5	1909	100.0	1909	10	US-09-951-535-3	Sequence 3, Appli
6	1909	100.0	1909	17	US-10-224-574-11	Sequence 11, Appl
7	1865.4	97.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
8	1836.6	96.2	2817	9	US-09-951-536-1	Sequence 1, Appli
9	1836.6	96.2	2817	9	US-09-963-521-1	Sequence 1, Appli
10	1836.6	96.2	2817	9	US-09-834-721-1	Sequence 1, Appli
11	1836.6	96.2	2817	9	US-09-783-388-1	Sequence 1, Appli
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13	1836.6	96.2	2817	17	US-10-224-574-9	Sequence 9, Appli
14	1590	83.3	1590	16	US-10-627-476-557	Sequence 557, App
15	1590	83.3	1590	16	US-10-450-055-41	Sequence 41, Appl
16	1503	78.7	1503	9	US-09-738-626-2884	Sequence 2884, Ap
17	615.4	32.2	3010	13	US-10-058-945-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-951-536-3
; Sequence 3, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrE-Gen
US-09-951-536-3

Query Match 100.0%; Score 1909; DB 9; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
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Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
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; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10

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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
US-09-963-521-3

  Query Match           100.0%;  Score 1909;  DB 9;  Length 1909;
  Best Local Similarity  100.0%;  Pred. No. 0;
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Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
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Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
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Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320

Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440

Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500

Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560

Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620

Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860

Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909


RESULT 3
US-09-834-721-3
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; Sequence 3, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
;  APPLICANT: RIEPING, MECHTHILD
;  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
;  FILE REFERENCE: 21123/280169/MAS
;  CURRENT APPLICATION NUMBER: US/09/834,721
;  CURRENT FILING DATE:  2001-04-16
;  PRIOR APPLICATION NUMBER: DE 100 26 494.8
;  PRIOR FILING DATE: 2000-05-27
;  PRIOR APPLICATION NUMBER: DE 101 02 823.7
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   OTHER INFORMATION: ATCC13032
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE gene
US-09-834-721-3

  Query Match             100.0%;  Score 1909;  DB 9;  Length 1909;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120

Qy        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Qy        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240
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Db        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240

Qy        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300

Qy        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360

Qy        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
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Db        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420

Qy        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Qy        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Qy        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
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Db        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600

Qy        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660

Qy        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
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Db        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720

Qy        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780
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Db        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780

Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840

Qy        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960

Qy        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020

Qy       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Qy       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140

Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
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Db       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200

Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320

Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440

Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
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Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500

Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560

Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620

Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
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Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCCAC 1860
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Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCCAC 1860

Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
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Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909


RESULT 4
US-09-783-388-3
; Sequence 3, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
;  APPLICANT: Ziegler, Petra
;  APPLICANT:  Eggeling, Lothar
;  APPLICANT:  Sahm, Hermann
;  APPLICANT:  Thierbach, Georg
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR
;  TITLE OF INVENTION:  ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/277066
;  CURRENT APPLICATION NUMBER: US/09/783,388
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum ATCC13032
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
US-09-783-388-3

  Query Match             100.0%;  Score 1909;  DB 9;  Length 1909;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60
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Db          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120

Qy        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Qy        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240

Qy        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300

Qy        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360

Qy        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
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Db        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420

Qy        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Qy        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Qy        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
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Db        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600

Qy        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
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Db        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660

Qy        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
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Db        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720

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Db        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780

Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
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Db        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840

Qy        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
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Db        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
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Db        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960

Qy        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
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Db        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020

Qy       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
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Db       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Qy       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
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Db       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140

Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
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Db       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200

Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
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Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320

Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
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Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
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Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500

Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
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Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620

Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860

Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909


RESULT 5
US-09-951-535-3
; Sequence 3, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT:  EGGELING, LOTHAR
;  APPLICANT:  SAHM, HERMANN
;  APPLICANT:  THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282415/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,535
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: DE 199 41 478.5
;  PRIOR FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
US-09-951-535-3

  Query Match           100.0%;  Score 1909;  DB 10;  Length 1909;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120

Qy        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Qy        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240

Qy        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300

Qy        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360

Qy        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420

Qy        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Qy        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Qy        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600

Qy        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660

Qy        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720

Qy        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780

Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840

Qy        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960

Qy        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020

Qy       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Qy       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140

Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200

Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320

Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440

Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500

Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560

Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620

Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860

Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909


RESULT 6
US-10-224-574-11
; Sequence 11, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
;  APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
;  APPLICANT:  P. Peters- Wendisch
;  TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
;  TITLE OF INVENTION:  L-Serin, improved process for the microbial manufacture of L-ser
;  TITLE OF INVENTION:  genetically modified microorganism suitable for the process.
;  FILE REFERENCE: FZJ-9912-PCT
;  CURRENT APPLICATION NUMBER: US/10/224,574
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: C. glutanicum ATCC 13 032
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thr E  (Threonin-exportcarrier)
US-10-224-574-11

  Query Match             100.0%;  Score 1909;  DB 17;  Length 1909;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCCCCCCTTTGACCTGGTGTTATTGA 60

Qy         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120

Qy        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Qy        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTG 240

Qy        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300

Qy        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360

Qy        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCGAGAATT 420

Qy        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Qy        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Qy        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGGC 600

Qy        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660

Qy        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCCT 720

Qy        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCAATGATGGGTGGTGCTGTTGCT 780

Qy        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840

Qy        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGT 960

Qy        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTG 1020

Qy       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Qy       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140

Qy       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT 1200

Qy       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCG 1320

Qy       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTG 1440

Qy       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCC 1500

Qy       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560

Qy       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620

Qy       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCAC 1860

Qy       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909


RESULT 7
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

  Query Match             97.7%;  Score 1865.4;  DB 9;  Length 3309400;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1866;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
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Db    2790740 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 2790799

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790800 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 2790859

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790860 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 2790919

Qy        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790920 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 2790979

Qy        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790980 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 2791039

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791040 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 2791099

Qy        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791100 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 2791159

Qy        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791160 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 2791219

Qy        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791220 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 2791279

Qy        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791280 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 2791339

Qy        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791340 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 2791399

Qy        698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791400 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 2791459

Qy        758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791460 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 2791519

Qy        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Db    2791520 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 2791579

Qy        878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791580 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 2791639

Qy        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791640 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 2791699

Qy        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791700 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 2791759

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791760 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 2791819

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791820 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 2791879

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791880 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 2791939

Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2791940 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 2791999

Qy       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792000 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 2792059

Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792060 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 2792119

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792120 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 2792179

Qy       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792180 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 2792239

Qy       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792240 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 2792299

Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792300 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 2792359

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792360 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 2792419

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792420 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 2792479

Qy       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792480 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 2792539

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792540 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2792599

Qy       1898 GCCGGGG 1904
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Db    2792600 GCCGGTG 2792606
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RESULT 8
US-09-951-536-1
; Sequence 1, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT:  EGGELING, LOTHAR
;  APPLICANT:  SAHM, HERMANN
;  APPLICANT:  THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282414/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,536
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (398)..(1864)
;   OTHER INFORMATION: thrE-Gen
US-09-951-536-1

  Query Match             96.2%;  Score 1836.6;  DB 9;  Length 2817;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
              | ||||||| |||||||||| |||||||||||||| ||  ||||||| ||||| ||||
Db        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

Qy        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Db        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |
Db        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

Qy        698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875

Qy        758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817
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Db        876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935

Qy        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Db        936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995

Qy        878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055

Qy        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
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Db       1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115

Qy        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
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Db       1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
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Db       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

Qy       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475

Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595

Qy       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Qy       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904
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Db       2016 GCCGGTG 2022
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RESULT 9
US-09-963-521-1
; Sequence 1, Application US/09963521
; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-963-521-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
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Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
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Db        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Db        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Db        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

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Qy        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Db        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697

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Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

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Db       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

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Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Db       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

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Db       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897

Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904

Db       2016 GCCGGTG 2022
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RESULT 10
US-09-834-721-1
; Sequence 1, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE gene
US-09-834-721-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
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Qy       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
Db       276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
Db       336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy       278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
Db       396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy       338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
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Qy       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
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Qy       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
Db       696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy       638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
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Qy       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
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Db      1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
Db       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
Db       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
Db       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
Db       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

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Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
Db       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
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Qy       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
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Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
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Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
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Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904
Db       2016 GCCGGTG 2022
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RESULT 11
US-09-783-388-1
; Sequence 1, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
;  APPLICANT: Ziegler, Petra
;  APPLICANT:  Eggeling, Lothar
;  APPLICANT:  Sahm, Hermann
;  APPLICANT:  Thierbach, Georg
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR
;  TITLE OF INVENTION:  ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/277066
;  CURRENT APPLICATION NUMBER: US/09/783,388
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum ATCC14752
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (398)..(1864)
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US-09-783-388-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy        38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy        98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
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Qy       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
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Db       276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
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Qy       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
             | |||||||| |||||||||| |||||||||||||| || |||||||| ||||| ||||
Db       576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

Qy       518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy       578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Db       756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

Qy       698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
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Qy       818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Qy       998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
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Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
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Db       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Qy       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904
              ||||| |
Db       2016 GCCGGTG 2022
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RESULT 12
US-09-951-535-1
; Sequence 1, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE

```
;  TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282415/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,535
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: DE 199 41 478.5
;  PRIOR FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (398)..(1864)
;   OTHER INFORMATION: thrE-Gen
US-09-951-535-1

  Query Match             96.2%;  Score 1836.6;  DB 10;  Length 2817;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
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Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
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Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
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Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
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Db        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
              | |||||||| |||||||||| |||||||||||||| ||  |||||||| ||||| ||||
Db        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

Qy        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
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Db        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
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Db        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

Qy        698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875

Qy        758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935

Qy        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Db        936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995

Qy        878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055

Qy        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115

Qy        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

Qy       1298 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1357
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Db       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475

Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
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Db       1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595

Qy       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Qy       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
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Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904
                |||||  |
Db       2016 GCCGGTG 2022


RESULT 13
US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
;  APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
;  APPLICANT:  P. Peters- Wendisch
;  TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
;  TITLE OF INVENTION:  L-Serin, improved process for the microbial manufacture of L-ser
;  TITLE OF INVENTION:  genetically modified microorganism suitable for the process.
;  FILE REFERENCE: FZJ-9912-PCT
;  CURRENT APPLICATION NUMBER: US/10/224,574
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: C. glutamicum ATCC 14 752
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (398)..(1867)
;   OTHER INFORMATION: thr E  (Threonin-exportcarrier)
US-10-224-574-9

  Query Match             96.2%;  Score 1836.6;  DB 17;  Length 2817;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
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Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
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Db        216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
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Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy        218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
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Db        336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy        278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
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Db        396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy        398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 457
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Db        516 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy        458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517
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Db        576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635

Qy        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 577
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Db        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy        578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Db        696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy        638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC 697
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |
Db        756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815

Qy        698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 757
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGG 875

Qy        758 CAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 817
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Db        876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTG 935

Qy        818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995

Qy        878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 937
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Db        996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055

Qy        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115

Qy        998 TTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCG 1057
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Db       1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG 1175

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177
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Db       1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy       1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237
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Db       1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355

Qy       1238 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
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Db       1356 CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415

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Db       1416 TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCT 1475

Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1417
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Db       1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGAT 1535

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1477
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Db       1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAG 1595

Qy       1478 CAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
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Db       1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy       1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGA 1715

Qy       1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1717
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Db       1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAA 1835

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
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Db       1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1895

Qy       1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
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Db       1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy       1898 GCCGGGG 1904
              ||||| |
Db       2016 GCCGGTG 2022
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RESULT 14
US-10-627-476-557
; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-10-627-476-557

Query Match 83.3%; Score 1590; DB 16; Length 1590;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 60

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Qy       1320 GTTTTATTACCTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGCTGCGATTGCTGCAAC 1379
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Qy       1440 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGC 1499
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RESULT 15
US-10-450-055-41
; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
;  APPLICANT: BASF Aktiengesellschaft
;  TITLE OF INVENTION: No. US20040043953A1el genes of Corynebacterium
;  FILE REFERENCE: 936_2000
;  CURRENT APPLICATION NUMBER: US/10/450,055
;  CURRENT FILING DATE:  2003-06-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
;   LENGTH: 1590
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1567)
;   OTHER INFORMATION: RXS00349
US-10-450-055-41

  Query Match             83.3%;  Score 1590;  DB 16;  Length 1590;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1590;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Job time : 1012.85 secs